We use cookies to ensure that we deliver the best user experience of our website. If you would like to, you can change your cookie settings at any time. Continue

Professor Zewei Luo PhD

Professor of Statistical Genetics and International Student Tutor

School of Biosciences (/schools/biosciences/index.aspx)

Contact details

Telephone +44 (0)121 41 45404 (Office) (tel:+44 121 41 45404)

Telephone (2) +44 (0)121 414 5460 (Lab) (tel:+44 121 414 5460)

Fax +44 (0)121 41 45925

Email z.luo@bham.ac.uk (mailto:z.luo@bham.ac.uk)

School of Biosciences
University of Birmingham
Edgbaston
Birmingham
B15 2TT
UK

About

Professor Zewei Luo is one of the world's foremost experts in the field of Statistical Genetics. Research of his team has been focused on genetics of quantitative traits through theoretical and empirical approaches.

Qualifications

BSc in Agronomy 1982, Southwest China Agricultural College, Chongqing
Diploma in Mathematics 1982, Southwest China Normal College, Chongqing
MSc in Quantitative Genetics 1985 Southwest China Agricultural College, Chongqing
PhD in Genetics 1989 The University of Birmingham, UK. Supervisor: Prof. M.J. Kearsey

Biography

Zewei Luo was initially trained as a quantitative geneticist at the University of Birmingham under supervision of Professor Michael J. Kearsey. He then worked as postdoctoral scientist in several UK institutions including University College London, University of Edinburgh with Professor Nick Barton and the Roslin Institute with Professor Robin Thompson during which time he gained experience in population genetics and statistical genetics. He was appointed to Institute of Genetics and Biostatistics in Fudan University (Shanghai China) and then joined the school of Biosciences at the University of Birmingham the United Kingdom.

Teaching

Director to MSc course in Analytical Genomics. Teaches Biostatistics, Population and Quantitative Genetics and Genomics in undergraduate 3rd year modules and master courses.

Postgraduate supervision

For a list of possible PhD projects offered by Professor Luo:

www.findaphd.com/search/customlink.asp?inst=birm-Biol&supersurname=Lu (http://www.findaphd.com/search/customlink.asp?inst=birm-Biol&supersurname=Luo)

Research

Research Theme within School of Biosciences: **Molecular and Cell Biology (/research/activity/cellbiology/index.aspx)**

Statistical Genetics

My research field is in Quantitative and Population Genetics, with major research interests in understanding the genetic architectures and mechanisms that underlie quantitative genetic variations, using both theoretical and experimental approaches. Our recent projects include:

Development of theoretical and experimental strategies for dissecting complex traits

Dissection of polygenic variation at molecular level has been a long standing target in classical genetics but still a challenging task in modern genomics. Although the last two decades have witnessed the dominance of research on mapping quantitative trait loci (QTL) in man, animal and plant species, the mapping precision and resolution that leads itself to molecular cloning of the target genes has remained a rare event. This project develops theoretical approaches for mapping and identifying the major effect genes that contribute to phenotypic variation of polygenic traits through altered coding sequence or expression of the genes. We have established an experimental model with budding yeast (S. cerevisiae) to dissect genic and transcriptional regulation network that affects natural variation in ethanol tolerance through integrating genomic, transcripteomic and proteomic information.

Theoretical modeling and prediction of marker-QTL linkage disequilibrium in natural populations

Association study has proven to be a powerful approach to isolate the oligo-genic basis of inherited diseases in humans and many other inherited characters in animal/plant species which segregate according to simple Mendelian rules. To extend the basic principle to complex traits, where the underlying genotype is no longer inferable directly from the corresponding phenotype, we are developing statistical approaches for modelling and predicting linkage disequilibria between genetic marker loci and loci affecting a complex trait in populations with various genetic structures.

Theory and methods for reconstructing genetic linkage maps in autotetraploid species

Construction of genetic linkage maps is usually the first milestone in launching a genome project for an organism. In the era of genomics, genetic linkage maps are now available or quickly becoming available in humans and in almost all important animal and plant species. In sharp contrast, the corresponding study in polyploid species is

theoretically challenging and still in its infancy. Our research on this topic focuses on developing theory and statistical approaches for genetic map construction and for modelling population genetic data in autotetraploid species, an example of which is cultivated potato, the world fourth most important food crop and the world food of future.

Evolutionary comparative genomics

Taking advantage of rapidly accumulating databases of genome studies and the datasets collected from our own experiments, we investigate the process and molecular mechanisms driving the divergent evolution of duplicate genes in the yeast protein-protein interaction network, the evolution of enzymatic genes in the yeast metabolic network, and the expression divergence between duplicate genes in the yeast genome.

Molecular aetiology of human inherited diseases

Working with our collaborators in Fudan University (Shanghai, China), we carried out experimental analyses to understand the molecular and/or cellular bases for non-small cell lung cancer (NSCLC), partial androgen receptor insensitivity syndrome and non-tuberculosis mycobacterium infection. Armed with these skills and our theoretical power, we are now able to study quantitative traits on the basis of integrating these powers.

Publications

Selected Publications Since 2004 (*-- Corresponding Authorship)

Theoretical and Methodological Research

1. Leach JL, L Wang, MJ Kearsey and **ZW Luo*.** (2010) Multilocus tetrasomic linkage analysis using Hidden Markov chain model. *Proc. Natl. Acad. Sci. USA*. **107**: 4270-4274.
2. Minghui Wang, Tianye Jia, Ning Jiang, Lin Wang, Xiaohua Hu and **Zewei Luo*** (2010) Inferringalinkage disequilibrium from non-random samples. *BMC Genomics* **11**: 328-340.
3. Wang MH, XH Hu, G Li, Lindsey J Leach, E Potokina, A Druka, R. Waugh, M J Kearsey and **ZW Luo*** (2009) Robust Detection and Genotyping of Single Feature Polymorphisms from Gene Expression Data. *PLoS Computational Biology* **5(3**) e1000317.
4. Jiang N, Leach LJ, Hu X, Potokina E, Jia T, Druka A, Waugh R, Kearsey MJ, **Luo ZW***. (2008). Methods for evaluating gene expression from Affymetrix microarray datasets. *BMC Bioinformatics.* **9**: 284.
5. **Luo ZW**, E Potokina, A Druka, R. Waugh and MJ Kearsey (2007). SFP genotyping from Affymetrix arrays is robust but largely detects cis-acting expression regulators. *Genetics*, **176**: 789-800.
6. Leach LJ, Zhang Z, Lu CQ, Kearsey MJ and **ZW Luo*** (2007). **The Role of *Cis*-Regulatory Motifs and Genetical Control of Expression in the Divergence of Yeast Duplicate Genes.** *Molecular Biology and Evolution* **24**: 2556-65.
7. **Luo ZW***, Ze Zhang, RM Zhang, M Pandey, O Gailing, Hans H. Hattemer and R Finkelday (2006) Modeling population genetic data in autotetraploid species. *Genetics* **172**: 639-646.
8. **Luo ZW*** , Ze Zhang, L Leach, RM Zhang, JE Broadshaw and MJ Kearsey (2006) Constructing genetic linkage maps under a tetrasomic model. *Genetics* 172: 2635-45.
9. **Luo ZW***, RM Zhang and MJ Kearsey (2004) Theoretical basis for genetic linkage analysis in autotetraploid species. *Proc. Natl. Acad. Sci. USA* 101: 7040-45.
10. **Luo ZW*** and L Ma (2004) An improved formulation of genetic heterozygosity in recurrent selection and backcross breeding schemes. *Genetical Research* 83: 49-53.

Empirical and Experimental Research

11. Chenqi Lu, Xiaohua Hu, Guiying Wang, L. J. Leach, Shengjie Yang, M. J. Kearsey and **Z.W. Luo*** (2010)Why do essential proteins tend to be clustered in the yeast interactome network? *Molecular BioSystems* **6**: 871-877.
12. James Cockram, Jon White, Diana L. Zuluaga, David Smith, Jordi Comadran, Malcolm Macaulay, **Zewei Luo**, Mike J. Kearsey, Peter Werner, David Harrap, Chris Tapsell, Hui Liu, Peter E. Hedley, Nils Stein, Daniela Schulte, Burkhard Steuernagel, David F. Marshall, William T. B. Thomas, Luke Ramsay, Ian Mackay, David J. Balding, The AGOUEB Consortium, Robbie Waugh, and Donal M. O'Sullivan (2010) Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. *Proc. Natl. Acad. Sci. USA* **107**: 21611-16.
13. Arnis Druka, Ilze Druka, Arthur G Centeno, Hongqiang Li, Zhaohui Sun, William T.B. Thomas, Nicola Bonar, Brian J Steffenson, Steven E Ullrich, Andris Kleinhofs, Roger P Wise, Timothy J Close, Elena Potokina, **Zewei Luo**, Carola Wagner, Günther F Schweizer, David F Marshall, Michael J Kearsey, Robert W Williams and Robbie Waugh (2008). Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. *BMC Genetics* **9**: 73.
14. Arnis Druka, Elena Potokina, **Zewei Luo**, Ning Jiang, Xinwei Chen, Mike Kearsey and Robbie Waugh (2009) Expression quantitative trait loci analysis in plants. *Plant Biotechnology Journal* **8**: 10-27.
15. Potokina E, Druka A, **Luo ZW,** Wise R, Waugh R and Kearsey M. (2008) eQTL analysis of 16,000 barley genes reveals a complex pattern of genome wide transcriptional regulation. *The Plant Journal* **53**: 90-101.
16. Potokina E, Druka A, Luo Z, Moscou M, Wise R, Waugh R, Kearsey M. (2008). Tissue dependent limited pleiotropy affects gene expression in barley. *Plant Journal* **56**: 287-296.
17. Druka, A; Potokina, E; Luo, Z, et al. (2008). Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen Puccinia graminis f. sp tritici in barley. *Theor Appl Genet*. **117**: 261-272.
18. Wang GY, Lu CQ, Zhang RM, Hu XH and **ZW Luo*** (2008). The E-cadherine gene polymorphisms -160C/A and Cancer Risk: A HuGE review and meta-analysis of 26 case-control studies. *American Journal of Epidemiology* **167**: 7-14.
19. Wang, YL; Zhang, RM; Luo, ZW, et al. (2008) High frequency of level II-V lymph node involvement in RET/PTC positive papillary thyroid carcinoma. *EJSO*, **31**: 77-81.
20. Wang GY, Zhang R, Hu XH, Lu CQ, Su CC, Luo SJ and **ZW Luo*** (2008) Promoter-hypermethylation associated defective expression of E-cadherin in primary non-small cell lung cancer. *Lung Cancer* **62**: 162-172.
21. Hu XH, MH Wang, T Tan, JR Li, H Yang, L Lindsey, RM Zhang and **ZW Luo*** (2007) Genetic dissection of ethanol tolerance in budding yeast *S. cerevisiea. Genetics* 175(3): 1479-88.
22. Wang GY, RM Zhang, XH Hu, L Leach and **ZW Luo*** (2007) TGF-b ligands, TGF-b receptors, and lung cancer. In *Cancer Drug Discovery and Development: Transforming Growth Factor-b in Cancer Therapy* Edited by S. B. Jakowlew. Humana Press, Totowa, NJ.
23. Wang J, MH Wang, RM Zhang, Z Zhao and **ZW Luo*** (2007) A chemiluminescence-based assessment of androgen binding activity in a large pedigree affected with androgen insensitivity syndrome. *The Journal of Biological and Chemical Luminescence* **22**: 370-378.
24. CQ Lu, Ze Zhang, L Lindsey, MJ Kearsey and **ZW Luo*** (2007) Impacts of yeast metabolic network structure on enzyme evolution. *Genome Biology* **8**: 407.
25. Hackett CA, I Milne, J Bradshaw and **ZW Luo** (2007) TetraploidMap for Windows: linkage map construction and QTL mapping in autotetraploid species. *J. Heredity* **98**: 927-929.
26. Pallett DW, Cooper JI, Wang H, Reeves J, **Luo ZW**, Machado RM, Obermeier C, Walsh JA and Kearsey MJ. (2007) Variation in the pathogenicity of two Turnip

Mosaic Virus isolates in wild UK Brassica rapa provenances. *Plant Pathology* **57**: 401-407.

27. Xu, L, H Chen, XH Hu, RM Zhang, Ze Zhang and **ZW Luo*** (2006). Average gene length is highly conserved in prokaryotes and eukaryotes and diverges only between the two kingdoms. *Mol. Biol. Evol.* 23: 1107-08.

28. Wang J, CC Su, JB Xu, LZ Chen, XH Hu, GY Wang, H Yang, Q Huang, SB Fu, P Li, RM Zhang and **ZW Luo*** (2006) Novel microdeletion in the transforming growth factor b type II receptor gene is associated with giant and large cell variants of nonsmall cell lung carcinoma. *Genes Chromosomes and Cancer* 46(2): 192-201.

29. Wang M., J Wang, Z Zhang, Z Zhao, RM Zhang, XH Hu, T. Tan, S. Luo and **ZW Luo*** (2005) Dissecting phenotypic variation among AIS patients. *Biochemical and Biophysical Research Communication* 335: 335-342.

30. **Luo ZW*** and Ze Zhang (2005). Commentary on Wu and Ma. *Genetics* 171: 21149-50.

31. Zhang Z, **ZW Luo***, H Kishino and MJ Kearsey (2004). Divergence pattern of duplicate genes in protein-protein interactions follows the power law. *Mol. Biol. Evol.* 22: 501-505.

32. Zhang HT, XF Chen, MH Wang, JC Wang, QY Qi, RM Zhang, WQ Xu, QY Fei, QQ Cheng, F Chen, CS Zhu, SH Tao and **ZW Luo**$ (2004) Defective expression of TGFbRII is associated with CpG methylated promoter in primary non-small cell lung cancer. *Clinical Cancer Research* 10: 2359-67.

33. Wan DF, M He, JR Wang, XK Qiu, W Zhou, **ZW Luo**, JG Chen and JR Gu (2004) Two variants of the human hepatorcellular carcinoma-associate HCAPI gene and their effects on the growth of the human liver cancer cell line Hep3B. *Genes Chromosomes & Cancer* **39**: 48-58.

© University of Birmingham 2014